



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 222738

TO: Minh-Tam Davis  
Location: REM/3A24/3C18  
Art Unit: 1642  
Wednesday, April 25, 2007

Case Serial Number: 10/728019

From: Deirdre Arnold  
Location: Biotech-Chem Library  
REM 1A55  
Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

### Search Notes

The Oct 1996 version of this sequence has 672 aa; the record and alignment are attached.

**These results will not appear on SCORE.**

*Please feel free to contact me if you have any questions or would like to rework the search.*

Thank you for using STIC services.

Regards,  
Deirdre Arnold





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UniProtKB/TrEMBL  
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UniSave/Batch

EBI UniProt UniSave

The UniProtKB Sequence/Annotation Version Archive (UniSave) is a repository of UniProtKB/Swiss-Prot and UniProtKB/TrEMBL entry versions.

Primary accession number or entry name: **P53349**

Go!

Date:  day-month-year (e.g. 30-11-1998 or 30-NOV-1998) or year-month

Save

UniProtKB

P53349

Later &gt;&gt;

Release: 34.0 Date: 01-OCT-1996

ID MEKK\_MOUSE STANDARD; PRT; 672 AA.  
AC P53349  
DT 01-OCT-1996 (REL. 34, CREATED)  
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
DE MEK KINASE (EC 2.7.1.-) (MEKK).  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C; TISSUE=BRAIN;  
RX MEDLINE; 93227040.  
RA LANGE-CARTER C.A., PLEIMAN C.M., GARDNER A.M., BLUMER K.J.,  
RA JOHNSON G.L.;  
RL SCIENCE 260:315-319(1993).  
CC -!- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE MAP KINASE KINASE 1  
CC (MEK1) WHICH LEADS TO PHOSPHORYLATION OF MAP KINASES.  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HEART AND SPLEEN  
CC A LOWER LEVEL EXPRESSION IS SEEN IN THE LIVER.  
CC -!- PTM: AUTOPHOSPHORYLATED.  
CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-  
CC PROTEIN KINASES. BELONGS TO THE MAP KINASE KINASE KINASE FAM.  
CC -----  
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CC -----  
DR EMBL; L13103; G293730; -.  
KW TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;  
KW PHOSPHORYLATION.  
FT DOMAIN 403 672 PROTEIN KINASE (BY SIMILARITY).  
FT NP\_BIND 409 416 ATP (BY SIMILARITY).  
FT BINDING 432 432 ATP (BY SIMILARITY).  
FT ACT\_SITE 529 529 BY SIMILARITY.  
SQ SEQUENCE 672 AA; 72983 MW; 67CE46FE CRC32;  
MVTAVPAVFS KLVTMLNASG STHFTRMRRR LMAIADEVEI AEVIQLGVED TVDGHQDSL  
AVAPTSCLEN SSLEHTVHRE KTGKGLSATR LSASSEDISD RLAGVSVGLP SSTTTEQPK  
AVQTKGRPHS QCLNSSPLSH AQLMFPAPSA PCSSAPSVDP ISKHRPQAFV PCKIPASAP  
TQRKFSLQFQ RNCSEHRDSD QLSPVFTQSR PPPSSNIHRP KPSRPVPGST SKLGDATKS  
MTLDLGSASR CDSFPGGGN SGNVIPSDE TVFTPVEDKC RLDVNTLNS SIEDLLEAS  
PSSDTTVTFK SEVAVLSPEK AENDDTYKDD VNHNQCKEK MEAEVEEALA IAMAMSASQ  
ALPIVPQLQV ENGEDIIIIQ QDTPETLPGH TKAKQPYRED AEWLKGGQIG LGAFSSCYQ  
QDVGTTILMA VKQVTYVRNT SSEQEEVVEA LREEIRMMGH LNHPIIRML GATCEKSNI  
LFIEWMAGGS VAHLLSKYGA FKESVVINYT EQLLRGLSYL HENQIIHRDV KGANLLIDS  
GQRLRIADFG AAARLASKGT GAGEFQGQLL GTIAFMAPEV LRQQYGRSC DVWSVGCAL  
PVCCHPDRN PEGIGNHVA LKFAQCTMA DCTGSHGDC LKSNVDC LKQDPRDSC

EMACAKPPWN AEKHSNHLAL IFKIASATTA PSTPSHLSFG LRDVAVRLE LQPQDRPPI  
ELLKHPVFRT TW

//

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OM protein - protein search, using sw model

Run on: April 25, 2007, 10:13:58 ; Search time 1 Seconds  
(without alignments)  
1.003 Million cell updates/sec

Title: US-10-728-019-3  
Perfect score: 7732  
Sequence: 1 MAAAGDRASSGFFGAAAA.....PQDRPPSRELLKHPVFRITW 1493

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 672 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : new.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	3467	44.8	672	1 MEKKMOUSE01OCT1996 Entered [darnold]

ALIGNMENTS

RESULT 1  
MEKKMOUSE01OCT1996  
; Entered [darnold 25-Apr-07 10:06]  
MEKKMOUSE01OCT1996

Query Match 44.8%; Score 3467; DB 1; Length 672;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	822	MVTAVPAVFSKLVMTLNASGTHETRMRRRLMAIADEVEIAEVIQLGVEDTVDGHQDSIQ	881
Db	1	MVTAVPAVFSKLVMTLNASGTHETRMRRRLMAIADEVEIAEVIQLGVEDTVDGHQDSIQ	60
Qy	882	AVAPTSCLSENSLEHTVHREKTGKLSATRLSASSEDISDRLAGVSVGLPSSTTTEQPKP	941
Db	61	AVAPTSCLSENSLEHTVHREKTGKLSATRLSASSEDISDRLAGVSVGLPSSTTTEQPKP	120
Qy	942	AVQTKGRPHSQCLNSSPLSHAQLMFPAPSPCAPSPVPDISKRPQAFVFCCKIPSPSQ	1001
Db	121	AVQTKGRPHSQCLNSSPLSHAQLMFPAPSPCAPSPVPDISKRPQAFVFCCKIPSPSQ	180
Qy	1002	TORKESLQFQNCSEHRDSDOLSPVFTQSRPPPSNIHRPKPSRPVPGSTSKLGDATKSS	1061
Db	181	TORKESLQFQNCSEHRDSDOLSPVFTQSRPPPSNIHRPKPSRPVPGSTSKLGDATKSS	240
Qy	1062	MTLDLGSASRCDDSPGGGSGNNAVIPSDETFTPTVEDKCRLDVNTLNSSIEDLLEASM	1121